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Feline bodyweight: genetic aspects of food intake

Wichert, Brigitta ; Häring, T ; Dolf, G ; Trossen, J ; Haase, B

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ESVCN



European Society of
Veterinary & Comparative
Nutrition



Host: Department of Animal Physiology
Faculty of Animal Breeding and Biology
University of Technology and Life Sciences
in Bydgoszcz

CONGRESS PROCEEDINGS

16th Congress of the European Society of Veterinary and Comparative Nutrition

September 13-15, 2012
Bydgoszcz, Poland



PROGRAM


WEDNESDAY, SEPTEMBER 12, 2012
CITY HOTEL

19:00 - 21:30 Welcome Party, Early Registration

THURSDAY, SEPTEMBER 13, 2012
Opera NOVA House

8:00 Registration

ROOM: MANRU

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FRIDAY, SEPTEMBER 14, 2012

Opera NOVA House

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Chair: Ronald Corbee

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Nestle Purina Session

✠ Nestlé PURINA

ROOM: MANRU

Chair: Britta Dobenecker

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ROOM: FIDELIO

Chair: Annette Zeyner

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17:00 General Meeting ESVCN

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SATURDAY, SEPTEMBER 15, 2012
Opera NOVA House

ROOM: MANRU

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SESSION XI: Equine

ROOM: MANRU

Chair: Manfred Coenen

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14:00	Post Congress Tour, Toruń	

Feline bodyweight: genetic aspects of food intake

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Introduction: Obesity is an increasing problem in household cats. Obesity and obesity-associated diseases in companion animals are among the diseases with the fastest growing prevalence worldwide. Besides food intake, food composition, and low activity, genetic factors are also believed to influence the development of obesity in cats. A striking phenotypic difference was observed in our experimental cat population and a complex segregation analysis indicated a genetic influence.

Animals, material and methods: A total of 41 intact kittens from the breeding family of the Institute of Animal Nutrition of the Vetsuisse Faculty University of Zurich, were investigated. The kittens were fed with different kinds of commercial dry food for kittens ad libitum until the age of 8 months. At month eight the cats were classified into an overweight (BCS >6) and lean (BCS < 6) phenotype using BCS (Laflamme, 1997). From the BCS, confirmed by a dual energy x-ray absorptiometry, a segregation analysis was performed. In a next step 6 males of the overweight group and 6 males of the lean group were tested for their food intake at ad libitum feeding and their energy expenditure using indirect calorimetry. The animals belonging to our experimental cat population were analyzed using the feline Illumina 60k SNP genotyping microarray. Genotyping results were analysed using the -assoc option of plink.

Results and discussion: The results of the segregation indicated an inheritance either driven by a major gene model or a mixed inheritance model. Considering the fact that the mixed inheritance and the major gene model could not be distinguished and that the estimated heritability of 0.41 (± 0.06) is substantial, we hypothesize that at least one major gene together with a polygenic component are likely to be responsible for the observed phenotypic difference. Albeit not significant at a genome level, marker on chromosome D3 and C2 were associated with body condition score. The associated regions on chromosome D3 contain *MC4R* and *NPY1R* as positional candidate genes, while no obvious candidate gene could be identified in the associated region on chromosome C2. Associations for *MC4R* and *NPY1R* are very good in line with the results determined by the investigation of daily food intake. Cats with a higher body condition score were eating significantly more per meal and day and both receptors are known to be involved in the regulation of food intake. Although good candidate genes are located in the associated regions, further analyses are required to confirm the associated chromosomal regions and to reveal functional mutations.

Conclusion: Complex segregation analyses indicated the activity of autosomal recessive major gene with incomplete penetrance but with a possible polygenic component. A whole-genome SNP association mapping identified three loci associated with body condition score in the experimental cat population. Subsequent fine structure mapping identified positional candidate genes involved in the regulation of food intake. This means, a genetic connection to overweight and the associated gene loci were found in the cat population of the Institute of Animal Nutrition, Vetsuisse Faculty University of Zurich. However, the identification of the specific mutations need further work.

References : Laflamme, D.P., 1997 : Development and validation of a body condition score system for cats: a clinical tool. *Feline Practice* 25: 13-17

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